



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/887,569  
Source: OIPE  
Date Processed by STIC: 7/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer-Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/887, 569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                                  prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering                  use space characters, instead.
  
- 4      Non-ASCII              The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                                  ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                                  each n or Xaa can only represent a single residue. Please present the maximum number of each  
                                  residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0          A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)                     . Normally, PatentIn would automatically generate this section from the  
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                                  the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                                  Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)              (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  This sequence is intentionally skipped  
  
                                  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)              <210> sequence id number  
                                  <400> sequence id number  
                                  000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)              Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>          Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response                  scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                                  is Artificial Sequence
  
- 11      Use of <220>          Sequence(s)                      missing the <220> "Feature" and associated numeric identifiers and responses.  
                                  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                                  "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0          Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIKE

## RAW SEQUENCE LISTING.

DATE: 07/07/2001

PATENT APPLICATION: US/09/887,569

TIME: 14:35:35

Input Set : A:\SEQUENCE.txt

Output Set: N:\CRF3\07062001\I887569.raw

4 <110> APPLICANT: Moloney, Maurice M.  
 5 Habibi, Hamid R.  
 7 <120> TITLE OF INVENTION: Expression of Somatotropin in Plant Seeds  
 9 <130> FILE REFERENCE: 9369-183  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/887,569  
 C--> 12 <141> CURRENT FILING DATE: 2001-06-25  
 14 <150> PRIOR APPLICATION NUMBER: US 09/210,843  
 15 <151> PRIOR FILING DATE: 1998-12-15  
 17 <160> NUMBER OF SEQ ID NOS: 2  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1101  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: synthetic construct  
 26 <400> SEQUENCE: 1

Does Not Comply  
 Corrected Diskette Needed

— see item #10 on  
 ERROR SUMMARY SHEET.

C--> 27 atggcgagata cagctagagg aacccatcac gatatacatcg gcagagacca gtacccgatg 60  
 28 atggggccgag accgagacca gtaccagatg tccggacgag gatctgacta ctccaagtct 120  
 29 aggcagattg ctaaagctgc aactgctgtc acagctggtg gttccctcct tgttctctcc 180  
 30 agccttacct ttgttggaac tgtcatagct ttgactggtg caacacctct gctcgtttatc 240  
 31 ttcagcccaa tccttgtccc ggctctcatc acagttgcac tctcatcac cggttttctt 300  
 32 tcctctggag ggtttgcat tgcgctata accgttttct cttggattta caagtaogca 360  
 33 acgggagagc acccacaggg atcagacaag ttggacagtg caaggatgaa gttgggaagc 420  
 34 aaagctcagg atctgaaaga cagagctcag tactacggac agcaacatac tgggtgggaa 480  
 35 catgaccgtg accgtactcg tgggtggccag cacactactc tcgttccacg aggatccgac 540  
 36 aaccagcggc tcttcaataa tgcagtcatt cgtgtacaac acctgcacca gctggctgca 600  
 37 aaaatgatta acgactttga ggacagcctg ttgcctgagg aacgcagaca gctgagtaaa 660  
 38 atcttcctc tgtctttctg caattctgac tacattgagg cgctgctgg aaaagatgaa 720  
 39 acacagaaga gctctatgct gaagcttctt cgcactctct ttcacctcat tgagtctctg 780  
 40 gagttcccaa gccagtcctt gaggcggaacc gtctcaaaac gctgaccgt agggaaaccc 840  
 41 aaccagctca ctgagaagct ggccgacttg aaaatgggca tcagtgtgct catccaggca 900  
 42 tgtctcgatg gtcaaccaa catggatgat aacgactcct tgcgctgcc ttttgaggac 960  
 43 ttctacttga ccatggggga gaacaacctc agagagagct ttcgtctgct ggcttgcttc 1020  
 44 aagaaggaca tgcacaaagt cgagacctac ttgagggttg caaattgcag gagatccctg 1080  
 45 gattccaact gcacctgta g 1101

— make sure  
 nuclear acid  
 bases are lower  
 case.

47 <210> SEQ ID NO: 2  
 48 <211> LENGTH: 366  
 49 <212> TYPE: PRT  
 50 <213> ORGANISM: synthetic construct  
 52 <400> SEQUENCE: 2  
 53 Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp  
 54 1 5 10 15  
 56 Gln Tyr Pro Met Met Gly Arg Asp Arg Gln Tyr Gln Met Ser Gly  
 57 20 25 30  
 59 Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr  
 60 35 40 45  
 62 Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu  
 63 50 55 60

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Input Set : A:\SEQUENCE.txt

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```

65 Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
66 65 70 75 80
68 Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
69 85 90 95
71 Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
72 100 105 110
74 Phe Ser Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser
75 115 120 125
77 Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp
78 130 135 140
80 Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu
81 145 150 155 160
83 His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Leu Val Pro
84 165 170 175
86 Arg Gly Ser Asp Asn Gln Arg Leu Phe Asn Asn Ala Val Ile Arg Val
87 180 185 190
89 Gln His Leu His Gln Leu Ala Ala Lys Met Ile Asn Asp Phe Glu Asp
90 195 200 205
92 Ser Leu Leu Pro Glu Glu Arg Arg Gln Leu Ser Lys Ile Phe Pro Leu
93 210 215 220
95 Ser Phe Cys Asn Ser Asp Tyr Ile Glu Ala Pro Ala Gly Lys Asp Glu
96 225 230 235 240
98 Thr Gln Lys Ser Ser Met Leu Lys Leu Leu Arg Ile Ser Phe His Leu
99 245 250 255
101 Ile Glu Ser Trp Glu Phe Pro Ser Gln Ser Leu Ser Gly Thr Val Ser
102 260 265 270
104 Asn Ser Leu Thr Val Gly Asn Pro Asn Gln Leu Thr Glu Lys Leu Ala
105 275 280 285
107 Asp Leu Lys Met Gly Ile Ser Val Leu Ile Gln Ala Cys Leu Asp Gly
108 290 295 300
110 Gln Pro Asn Met Asp Asp Asn Asp Ser Leu Pro Leu Pro Phe Glu Asp
111 305 310 315 320
113 Phe Tyr Leu Thr Met Gly Glu Asn Asn Leu Arg Glu Ser Phe Arg Leu
114 325 330 335
116 Leu Ala Cys Phe Lys Lys Asp Met His Lys Val Glu Thr Tyr Leu Arg
117 340 345 350
119 Val Ala Asn Cys Arg Arg Ser Leu Asp Ser Asn Cys Thr Leu
120 355 360 365

```

## VERIFICATION SUMMARY

DATE: 07/07/2001

PATENT APPLICATION: US/09/887,569

TIME: 14:35:36

Input Set : A:\SEQUENCE.txt

Output Set: N:\CRF3\07062001\I887569.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:27 M:112 C: (48) String data converted to lower case,

M:112 Repeated in SeqNo=1